

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

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(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 30-AUG-1991
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100
(B) TELEFAX: 619-455-5110

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DB60R32

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 130..1177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
15	CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA	120
	GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC	168
	Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe	
	1 5 10	
20	GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC	216
	Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys	
	15 20 25	
	AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG	264
	Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala	
	30 35 40 45	
25	GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC	312
	Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala	
	50 55 60	
30	AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC	360
	Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His	
	65 70 75	

	AAG	GGC	CTC	TTC	TGT	GAC	TTC	GGC	TCC	CCG	GCC	AAC	CGC	AAG	ATC	GGC	408
	Lys	Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	
			80					85					90				
5	GTG	TGC	ACC	GCC	AAA	GAT	GGT	GCT	CCC	TGC	ATC	TTC	GGT	GGT	ACG	GTG	456
	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	
		95					100					105					
	TAC	CGC	AGC	GGA	GAG	TCC	TTC	CAG	AGC	AGC	TGC	AAG	TAC	CAG	TGC	ACG	504
	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	
	110					115					120					125	
10	TGC	CTG	GAC	GGG	GCG	GTG	GGC	TGC	ATG	CCC	CTG	TGC	AGC	ATG	GAC	GTT	552
	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	
					130					135					140		
	CGT	CTG	CCC	AGC	CCT	GAC	TGC	CCC	TTC	CCG	AGG	AGG	GTC	AAG	CTG	CCC	600
15	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	
				145					150					155			
	GGG	AAA	TGC	TGC	GAG	GAG	TGG	GTG	TGT	GAC	GAG	CCC	AAG	GAC	CAA	ACC	648
	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	
			160					165					170				
	GTG	GTT	GGG	CCT	GCC	CTC	GCG	GCT	TAC	CGA	CTG	GAA	GAC	ACG	TTT	GGC	696
20	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	
		175					180					185					
	CCA	GAC	CCA	ACT	ATG	ATT	AGA	GCC	AAC	TGC	CTG	GTC	CAG	ACC	ACA	GAG	744
	Pro	Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	
	190					195					200					205	
	TGG	AGC	GCC	TGT	TCC	AAG	ACC	TGT	GGG	ATG	GGC	ATC	TCC	ACC	CGG	GTT	792
25	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	
					210					215					220		
	ACC	AAT	GAC	AAC	GCC	TCC	TGC	AGG	CTA	GAG	AAG	CAG	AGC	CGC	CTG	TGC	840
30	Thr	Asn	Asp	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	
				225					230					235			
	ATG	GTC	AGG	CCT	TGC	GAA	GCT	GAC	CTG	GAA	GAG	AAC	ATT	AAG	AAG	GGC	888
	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	
			240					245					250				

	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936
	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu	
	255 260 265	
5	CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984
	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly	
	270 275 280 285	
	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032
	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu	
	290 295 300	
10	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080
	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met	
	305 310 315	
	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128
15	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn	
	320 325 330	
	GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T	1177
	Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
	335 340 345	
	GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACTGA TTCACATCTC	1237
20	ATTTTTCGGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG	1297
	GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC	1357
	CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC	1417
	CAGAAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT	1477
	CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA	1537
25	AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC	1597
	CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA	1657
	CATTCTGATT CGAATGACAC TGTTCAAGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT	1717
	TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAATATT	1777
	GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA	1837

AGTTGTTTGT GCCTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA 1897
 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957
 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA 2017
 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075

5 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1 5 10 15
 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 15 20 25 30
 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35 40 45
 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50 55 60
 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 20 65 70 75 80
 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 25 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125

	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro	
	130						135					140					
	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys	
	145					150					155					160	
5	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly	
					165					170					175		
	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro	
				180					185					190			
10	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala	
			195					200					205				
	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	
		210					215					220					
	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg	
	225					230					235					240	
15	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys	
					245					250					255		
	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly	
				260					265					270			
20	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	
			275					280					285				
	Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu	
		290					295					300					
	Phe	Lys	Cys	Pro	Asp	Gly	Glu	Val	Met	Lys	Lys	Asn	Met	Met	Phe	Ile	
	305					310					315					320	
25	Lys	Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	
					325					330					335		
	Glu	Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala				
				340					345								